

In the Claims

Claim 1-57 (Canceled)

58. (Currently Amended) A method of identifying a nucleotide sequence comprising comparing a target sequence to a sequence stored in computer readable medium having recorded thereon at least 100 nucleotide sequences including sequence selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905 and complements thereof, and identifying said target sequence as being present in the computer readable medium based on said comparison, wherein said target sequence is compared to at least one sequence selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905.

59. (Currently Amended) A method for identifying a nucleic acid sequence comprising:

- a) providing a target nucleotide sequence;
- b) comparing said target nucleotide sequence to one or more nucleotide sequences stored in a computer readable medium having recorded thereon at least 100 nucleotide sequences including sequences selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905 and complements thereof wherein said target nucleotide sequence is compared to at least one of said sequences selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905; and
- c) identifying said target nucleotide sequence as having significant sequence identity to said one or more nucleotide sequences stored in a computer readable medium based on said comparison.

60. (Previously presented) The method according to claim 59, wherein said target sequence shares between 100% and 90% sequence identity with one or more of said nucleotide sequences stored on a computer readable medium.

61. (Previously presented) The method according to claim 60, wherein said target sequence shares between 100% and 95% sequence identity with one or more of said nucleotide sequences stored on a computer readable medium.

62. (Previously presented) The method according to claim 61 wherein said target sequence shares between 100% and 98% sequence identity with one or more of said nucleotide sequences stored on a computer readable medium.

63. (Previously presented) The method according to claim 62 wherein said target sequence shares between 100% and 99% sequence identity with one or more of said nucleotide sequences stored on a computer readable medium.

64. (Previously presented) The method according to claim 59, wherein said target sequence is identified as homologous to an open reading frame (ORF) within said nucleotide sequence stored on a computer readable medium.

65. (Previously presented) The method of claim 59, wherein said target sequence is a nucleotide sequence of between about 30 and about 300 nucleotide residues in length.

66. (Previously presented) The method of claim 59, wherein said target sequence is identified as homologous to a sequence encoding an *Emericella nidulans* protein or fragment thereof within said one or more nucleotide sequences stored on a computer readable medium.

67. (Currently Amended) A method of detecting a nucleotide sequence comprising:

a) providing a target nucleotide sequence;

b) comparing said target nucleotide sequence to a nucleotide sequence stored in a computer readable medium having recorded thereon at least 100 nucleotide sequences including sequences selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905 and complements thereof, wherein said target sequence is compared to at least one sequence selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905; and

c) identifying said target sequence as homologous to said nucleotide sequence based on said comparison.

68. (Previously presented) The method according to claim 67, wherein said target sequence is homologous to an open reading frame (ORF) within said nucleotide sequence.

69. (Previously presented) The method of claim 67, wherein said target sequence is a nucleotide sequence of between about 30 and about 300 nucleotide residues in length.

70. (Previously presented) The method of claim 67, wherein said target sequence is identified according to degree of homology to said nucleotide sequence stored in a computer readable medium.

71. (Currently Amended) A method of ranking a target nucleotide sequence by homology to a nucleotide sequence of *E. nidulans* comprising:

a) providing a target nucleotide sequence;

b) comparing said target nucleotide sequence to a nucleotide sequence stored in a computer readable medium having recorded thereon at least 100 nucleotide sequences including sequences selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905 and complements thereof wherein said target nucleotide sequence is compared to at least one sequence selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905; and

c) ranking said target sequence ~~by degree of~~ based on percent homology to said nucleotide sequence of *E. nidulans*.

72. (Previously presented) The method of claim 71, wherein said target sequence is a nucleotide sequence of between about 30 and about 300 nucleotide residues in length.

73. (New) A method for identifying a nucleic acid sequence comprising:

a) providing a target nucleotide sequence;

b) comparing said target nucleotide sequence to one or more nucleotide sequences stored in a computer readable medium having recorded thereon at least 100 nucleotide sequences including sequences selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905 and complements thereof wherein said target nucleotide sequence is compared to at least one of said sequences selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905; and

c) identifying said target nucleotide sequence as having significant sequence identity to said one or more nucleotide sequences stored in a computer readable medium,

wherein said sequences stored in said computer readable medium function to facilitate said identification of said target sequence as having significant sequence identity.

74. (New) The method of claim 73, wherein said method identifies a nucleic acid sequence within the *Emericella nidulans* genome.

75. (New) The method of claim 73, wherein said target sequence shares between 100% and 90% sequence identity with one or more of said sequence selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905.

76. (New) The method of claim 75, wherein said target sequence shares between 100% and 95% sequence identity with one or more of said sequence selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905.

77. (New) The method of claim 76, wherein said target sequence shares between 100% and 98% sequence identity with one or more of said sequence selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905.

78. (New) The method of claim 77, wherein said target sequence shares between 100% and 98% sequence identity with one or more of said sequence selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905.

79. (New) A method for identifying the function of a plurality of fungal nucleic acid sequences by determining homology to a nucleotide sequence in the *Emericella nidulans* genome comprising:

- a) providing a plurality of target fungal nucleotide sequences;

b) comparing said target fungal nucleotide sequences to one or more *E. nidulans* nucleotide sequences stored in a computer readable medium having recorded thereon at least 100 nucleotide sequences including sequences selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905 and descriptions identifying encoded proteins wherein said target fungal nucleotide sequence is compared to at least one of said sequences selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905; and

c) identifying the function of said target nucleotide sequence based on homology to a nucleotide sequence in the *E. nidulans* genome based on said comparison, wherein said sequences are stored in said computer readable medium function to facilitate said identification.